

SEQUENCE LISTING

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OCT 15 2001
PATENT & TRADEMARK OFFICE
<110> Pausch, Mark H
Price, Laura A

<120> POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
AND METHODS OF USING SAME

<130> 01142.0122 SEQUENCE LISTING

<140> 08/816, 011
<141> 1997-03-11

Jul 6/2
<150> 08/332, 312
<151> 1994-10-31

<150> PCT/US95/14364
<151> 1995-10-25

<160> 67

<170> PatentIn Ver. 2.1

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<212> DNA
<213> Drosophila melanogaster

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<213> Drosophila melanogaster

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Lys Ile Ser Arg Ala Glu Gln Arg Lys Ala Gln Ile Ala Ile Asn Glu
35 40 45

Tyr Leu Leu Glu Glu Leu Gly Asp Lys Asn Thr Thr Thr Gln Asp Glu
50 55 60

Ile Leu Gln Arg Ile Ser Asp Tyr Cys Asp Lys Pro Val Thr Leu Pro
65 70 75 80

Pro Thr Tyr Asp Asp Thr Pro Tyr Thr Trp Thr Phe Tyr His Ala Phe
85 90 95

Phe Phe Ala Phe Thr Val Cys Ser Thr Val Gly Tyr Gly Asn Ile Ser
100 105 110

Pro Thr Thr Phe Ala Gly Arg Met Ile Met Ile Ala Tyr Ser Val Ile
115 120 125

Gly Ile Pro Val Asn Gly Ile Leu Phe Ala Gly Leu Gly Glu Tyr Phe
130 135 140

Gly Arg Thr Phe Glu Ala Ile Tyr Arg Arg Tyr Lys Lys Tyr Lys Met
145 150 155 160

Ser Thr Asp Met His Tyr Val Pro Pro Gln Leu Gly Leu Ile Thr Thr
165 170 175

Val Val Ile Ala Leu Ile Pro Gly Ile Ala Leu Phe Leu Val Leu Pro
180 185 190

Cys Val Gly Val His Leu Leu Arg Glu Leu Gly Leu Ser Ser Ile Ser
195 200 205

Leu Tyr Tyr Ser Tyr Val Thr Thr Thr Ile Gly Phe Gly Asp Tyr
210 215 220

Val Pro Thr Phe Gly Ala Asn Gln Pro Lys Glu Phe Gly Gly Trp Phe
225 230 235 240

Val Val Tyr Gln Ile Phe Val Ile Val Trp Phe Ile Phe Ser Leu Gly
245 250 255

Tyr Leu Val Met Ile Met Thr Phe Ile Thr Arg Gly Leu Gln Ser Lys
260 265 270

Lys Leu Ala Tyr Leu Glu Gln Gln Leu Ser Ser Asn Leu Lys Ala Thr
275 280 285

Gln Asn Arg Ile Trp Ser Gly Val Thr Lys Asp Val Gly Tyr Leu Arg
290 295 300

Arg Met Leu Asn Glu Leu Tyr Ile Leu Lys Val Lys Pro Val Tyr Thr
305 310 315 320

Asp Val Asp Ile Ala Tyr Thr Leu Pro Arg Ser Asn Ser Cys Pro Asp
325 330 335

Leu Ser Met Tyr Arg Val Glu Pro Ala Pro Ile Pro Ser Arg Lys Arg
340 345 350

Ala Phe Ser Val Cys Ala Asp Met Val Gly Ala Gln Arg Glu Ala Gly
355 360 365

Met Val His Ala Asn Ser Asp Thr Asp Leu Thr Lys Leu Asp Arg Glu
370 375 380

Lys Thr Phe Glu Thr Ala Glu Ala Tyr His Gln Thr Thr Asp Leu Leu
385 390 395 400

Ala Lys Val Val Asn Ala Leu Ala Thr Val Lys Pro Pro Pro Ala Glu
405 410 415

Gln Glu Asp Ala Ala Leu Tyr Gly Gly Tyr His Gly Phe Ser Asp Ser
420 425 430

Gln Ile Leu Ala Ser Glu Trp Ser Phe Ser Thr Val Asn Glu Phe Thr
435 440 445

Ser Pro Arg Arg Pro Arg Ala Arg Ala Cys Ser Asp Phe Asn Leu Glu
450 455 460

Ala Pro Arg Trp Gln Ser Glu Arg Pro Leu Arg Ser Ser His Asn Glu
465 470 475 480

Trp Thr Trp Ser Gly Asp Asn Gln Gln Ile Gln Glu Ala Phe Asn Gln
485 490 495

Arg Tyr Lys Gly Gln Gln Arg Ala Asn Gly Ala Ala Asn Ser Thr Met
500 505 510

Val His Leu Glu Pro Asp Ala Leu Glu Glu Gln Leu Arg Asn Asn His
515 520 525

Arg Val Pro Val Ala Ser Arg Ser Ser Pro Cys Arg Met Val Cys Asp
530 535 540

Val Cys Phe Pro Ser Arg Arg Ser Thr Pro Arg Arg Ile Trp Ser Ala
545 550 555 560

Ser Cys Pro Trp Ser Arg Tyr Pro Arg Val Ser Ser Arg Arg Lys Pro
565 570 575

Asp Pro Arg Trp Thr Thr Ser Thr Arg Ser Arg Arg Pro Pro Val
580 585 590

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Met Ala Ala Trp Pro Ala Ala Ala Gly

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<212> DNA

<213> *Caenorhabditis elegans*

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<213> *Drosophila melanogaster*

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Asn Glu Val Lys Lys Asn Ala Ala Thr Glu Thr Trp Thr Phe Ser Ser

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25

30

Ser Ile Phe Phe Ala Val Thr Val Val Thr Thr Ile Gly Tyr Gly Asn

35

40

45

Pro Val Pro Val Thr Asn Ile Gly Arg Ile Trp Cys Ile Leu Phe Ser

50

55

60

Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Ile Ala Asp Leu Ala Gly

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70

75

80

Lys Phe Leu Ser Glu His Leu Val Trp Leu Tyr Gly Asn Tyr Leu Lys
85 90 95

Leu Lys Tyr Leu Ile Leu Ser Arg His Arg Lys Glu Arg Arg Glu His
100 105 110

Val Cys Glu His Cys His Ser His Gly Met Gly His Asp Met Asn Ile
115 120 125

Glu Glu Lys Arg Ile Pro Ala Phe Leu Val Leu Ala Ile Leu Ile Val
130 135 140

Tyr Thr Ala Phe Gly Gly Val Leu Met Ser Lys Leu Glu Pro Trp Ser
145 150 155 160

Phe Phe Thr Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr Thr Val Gly
165 170 175

Phe Gly Asp Leu Met Pro Arg Arg Asp Gly Tyr Met Tyr Ile Ile Leu
180 185 190

Leu Tyr Ile Ile Leu Gly Lys Phe Ser Met Lys Lys Lys Gln Lys Phe
195 200 205

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Lys Ile Phe Leu Gly Leu Ala Ile Thr Thr Met Cys Ile Asp Leu Val
210 215 220

Gly Val Gln Tyr Ile Arg Lys Ile His Tyr Phe Gly Arg Lys Ile Gln
225 230 235 240

Asp Ala Arg Ser Ala Leu Ala Val Val Gly Gly Lys Val Val Leu Val
245 250 255

Ser Glu Leu Tyr Ala Asn Leu Met Gln Lys Arg Ala Arg Asn Met Ser
260 265 270

Arg Glu Ala Phe Ile Val Glu Asn Leu Tyr Val Ser Lys His Ile Ile
275 280 285

Pro Phe Ile Pro Thr Asp Ile Arg Cys Ile Arg Tyr Ile Asp Gln Thr
290 295 300

Ala Asp Ala Ala Thr Ile Ser Thr Ser Ser Ala Ile Asp Met Gln
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<213> *Caenorhabditis elegans*

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<213> *Caenorhabditis elegans*

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Drosophila melanogaster
<210> 7
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<212> PRT
<213> *Drosophila melanogaster*

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<210> 8
<211> 24
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<213> *Drosophila melanogaster*

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<213> Drosophila melanogaster

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Arg Tyr Ile Thr Asp His Cys Pro
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<210> 10
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<213> Drosophila melanogaster

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Ile Ser Pro Thr Thr Phe Ala Gly
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<211> 24
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<213> Drosophila melanogaster

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Ala Phe Trp Trp Ala Val Val Thr Met Thr Thr Val Gly Tyr Gly Asp
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Met Thr Pro Val Gly Phe Trp Gly
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<210> 12
<211> 24
<212> PRT
<213> Drosophila melanogaster

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Met Val Pro Glu Thr Ile Ala Gly
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<213> Drosophila m^élanogaster

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Ile Cys Pro Thr Thr Ala Leu Gly
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<210> 14
<211> 24
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Met Ala Pro Lys Thr Tyr Ile Gly
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<210> 15
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<213> Drosophila melanogaster

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Ala Leu Tyr Phe Thr Met Thr Cys Met Thr Ser Val Gly Phe Gly Asn
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Val Ala Ala Glu Thr Asp Asn Glu
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<210> 16
<211> 24
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<213> Drosophila melanogaster

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Cys Val Tyr Phe Leu Ile Val Thr Met Ser Thr Val Gly Tyr Gly Asp
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Val Tyr Cys Glu Thr Val Leu Gly
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<213> Drosophila melanogaster

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Tyr Val Pro Thr Phe Gly Ala Asn
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<212> PRT

<213> Drosophila melanogaster

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Ile Ser Pro Thr Thr Phe Ala Gly
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<210> 19

<211> 24

<212> PRT

<213> Drosophila melanogaster

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Ser Ile Phe Phe Ala Val Thr Val Val Thr Thr Ile Gly Tyr Gly Asn
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Pro Val Pro Val Thr Asn Thr Gly
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<213> Drosophila melanogaster

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Tyr Val Pro Thr Phe Gly Ala Asn
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<210> 21
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Leu Met Pro Arg Arg Asp Gly Tyr
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<213> Drosophila melanogaster

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<213> Drosophila melanogaster

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<210> 24
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<213> Drosophila melanogaster

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<210> 25

<211> 24

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<213> Drosophila melanogaster

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<210> 26

<211> 27

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<213> Drosophila melanogaster

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<213> Drosophila melanogaster

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<210> 28

<211> 27

<212> DNA

<213> Drosophila melanogaster

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<210> 29

<211> 24

<212> DNA

<213> Drosophila melanogaster

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<210> 30
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<213> Drosophila melanogaster

<400> 30
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<400> 31
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<210> 33
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<210> 35
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<213> Drosophila melanogaster

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<210> 36
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<213> Caenorhabditis elegans

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<211> 481
<212> PRT
<213> Drosophila melanogaster

<400> 37
Met Ser Pro Asn Arg Trp Ile Leu Leu Leu Ile Phe Tyr Ile Ser Tyr

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10

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20 25 30

Lys Ile Ser Arg Ala Glu Gln Arg Lys Ala Gln Ile Ala Ile Asn Glu
35 40 45

Tyr Leu Leu Glu Glu Leu Gly Asp Lys Asn Thr Thr Thr Gln Asp Glu
50 55 60

Ile Leu Gln Arg Ile Ser Asp Tyr Cys Asp Lys Pro Val Thr Leu Pro
65 70 75 80

Pro Thr Tyr Asp Asp Thr Pro Tyr Thr Trp Thr Phe Tyr His Ala Phe
85 90 95

Phe Phe Ala Phe Thr Val Cys Ser Thr Val Gly Tyr Gly Asn Ile Ser
100 105 110

Pro Thr Thr Phe Ala Gly Arg Met Ile Met Ile Ala Tyr Ser Val Ile
115 120 125

Gly Ile Pro Val Asn Gly Ile Leu Phe Ala Gly Leu Gly Glu Tyr Phe
130 135 140

Gly Arg Thr Phe Glu Ala Ile Tyr Arg Arg Tyr Lys Lys Tyr Lys Met
145 150 155 160

Ser Thr Asp Met His Tyr Val Pro Pro Gln Leu Gly Leu Ile Thr Thr
165 170 175

Val Val Ile Ala Leu Ile Pro Gly Ile Ala Leu Phe Leu Val Leu Pro
180 185 190

Cys Val Gly Val His Leu Leu Arg Glu Leu Gly Leu Ser Ser Ile Ser
195 200 205

Leu Tyr Tyr Ser Tyr Val Thr Ile Thr Thr Ile Gly Phe Gly Asp Tyr
210 215 220

Val Pro Thr Phe Gly Ala Asn Gln Pro Lys Glu Phe Gly Gly Trp Phe
225 230 235 240

Val Val Tyr Gln Ile Phe Val Ile Val Trp Phe Ile Phe Ser Leu Gly
245 250 255

Tyr Leu Val Met Ile Met Thr Phe Ile Thr Arg Gly Leu Gln Ser Lys

260

265

270

Lys Leu Ala Tyr Leu Glu Gln Gln Leu Ser Ser Asn Leu Lys Ala Thr
 275 280 285

Gln Asn Arg Ile Trp Ser Gly Val Thr Lys Asp Val Gly Tyr Leu Arg
 290 295 300

Arg Met Leu Asn Glu Leu Tyr Ile Leu Lys Val Lys Pro Val Tyr Thr
 305 310 315 320

Asp Val Asp Ile Ala Tyr Thr Leu Pro Arg Ser Asn Ser Cys Pro Asp
 325 330 335

Leu Ser Met Tyr Arg Val Glu Pro Ala Pro Ile Pro Ser Arg Lys Arg
 340 345 350

Ala Phe Ser Val Cys Ala Asp Met Val Gly Ala Gln Arg Glu Ala Gly
 355 360 365

Met Val His Ala Asn Ser Asp Thr Asp Leu Thr Lys Leu Asp Arg Glu
 370 375 380

Lys Thr Phe Glu Thr Ala Glu Ala Tyr His Gln Thr Thr Asp Leu Leu
 385 390 395 400

Ala Lys Val Val Asn Ala Leu Ala Thr Val Lys Pro Pro Pro Ala Glu
 405 410 415

Gln Glu Asp Ala Ala Leu Tyr Gly Gly Tyr His Gly Phe Ser Asp Ser
 420 425 430

Gln Ile Leu Ala Ser Glu Trp Ser Phe Ser Thr Val Asn Glu Phe Thr
 435 440 445

Ser Pro Arg Arg Pro Arg Ala Arg Ala Cys Ser Asp Phe Asn Leu Glu
 450 455 460

Ala Pro Arg Trp Gln Ser Glu Arg Pro Leu Arg Ser Ser His Asn Glu
 465 470 475 480

Trp

<210> 38

<211> 337

<212> PRT

<213> *Caenorhabditis elegans*

<220>

<221> UNSURE

<222> (337)

<223> X AT RESIDUE 337 IS AN UNKNOWN RESIDUE

<400> 38

Met Ser Asp Gln Leu Phe Val Ala Phe Glu Lys Tyr Phe Leu Thr Ser
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Asn Glu Val Lys Lys Asn Ala Ala Thr Glu Thr Trp Thr Phe Ser Ser
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Ser Ile Phe Phe Ala Val Thr Val Val Thr Thr Ile Gly Tyr Gly Asn
35 40 45

Pro Val Pro Val Thr Asn Ile Gly Arg Ile Trp Cys Ile Leu Phe Ser
50 55 60

Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Ile Ala Cys Leu Ala Gly
65 70 75 80

Lys Phe Leu Ser Glu His Leu Val Trp Leu Tyr Gly Asn Tyr Leu Lys
85 90 95

Leu Lys Tyr Leu Ile Leu Ser Arg His Arg Lys Glu Arg Arg Glu His
100 105 110

Val Cys Glu His Cys His Ser His Gly Met Gly His Asp Met Asn Ile
115 120 125

Glu Glu Lys Arg Ile Pro Ala Phe Leu Val Leu Ala Ile Leu Ile Val
130 135 140

Tyr Thr Ala Phe Gly Gly Val Leu Met Ser Lys Leu Glu Pro Trp Ser
145 150 155 160

Phe Phe Thr Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr Thr Val Gly
165 170 175

Phe Gly Asp Leu Met Pro Arg Arg Asp Gly Tyr Met Tyr Ile Ile Leu
180 185 190

Leu Tyr Ile Ile Leu Gly Lys Phe Ser Met Lys Lys Lys Gln Lys Phe
195 200 205

Lys Ile Phe Leu Gly Leu Ala Ile Thr Thr Met Cys Ile Asp Leu Val

210

215

220

Gly Val Gln Tyr Ile Arg Lys Ile His Tyr Phe Gly Arg Lys Ile Gln
225 230 235 240

Asp Ala Arg Ser Ala Leu Ala Val Val Gly Gly Lys Val Val Leu Val
245 250 255

Ser Glu Leu Tyr Ala Asn Leu Met Gln Lys Arg Ala Arg Asn Met Ser
260 265 270

Arg Glu Ala Phe Ile Val Glu Asn Leu Tyr Val Ser Lys His Ile Ile
275 280 285

Pro Phe Ile Pro Thr Asp Ile Arg Cys Ile Arg Tyr Ile Asp Gln Thr
290 295 300

Ala Asp Ala Ala Thr Ile Ser Thr Ser Ser Ala Ile Asp Met Gln
305 310 315 320

Ser Cys Arg Phe Cys His Ser Arg Tyr Ser Leu Asn Arg Ala Phe Lys
325 330 335

Xaa

1
int.
<210> 39

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DEGENERATE
PRIMER BASED ON HUMAN POTASSIUM CHANNELS

<220>

<221> variation

<222> (2)

<223> N AT BASE 2 INDICATES ANY NUCLEOTIDE

<400> 39

tnggatwygg wgaywyt

17

<210> 40

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DEGENERATE
PRIMER BASED ON HUMAN POTASSIUM CHANNELS

<400> 40

rtcwccrwah ccdaydgt

18

<210> 41

<211> 28

<212> DNA

<213> Homo sapiens

<400> 41

cgcaggcaga gccacaaaaga gtacacag

28

D
cont.
<210> 42

<211> 26

<212> DNA

<213> Homo sapiens

<400> 42

ggagatcagc taggcaccat atttgg

26

<210> 43

<211> 26

<212> DNA

<213> Homo sapiens

<400> 43

atgctgcattg cctcatgcattt cccagc

26

<210> 44

<211> 20

<212> DNA

<213> Homo sapiens

<400> 44

ggttatataa agagagggct

20

<210> 45

<211> 426

<212> PRT

<213> Homo sapiens

<400> 45

Met Leu Pro Ser Ala Ser Arg Glu Arg Pro Gly Tyr Arg Ala Gly Val
1 5 10 15

Ala Ala Pro Asp Leu Leu Asp Pro Lys Ser Ala Ala Gln Asn Ser Lys
20 25 30

Pro Arg Leu Ser Phe Ser Thr Lys Pro Thr Val Leu Ala Ser Arg Val
35 40 45

Glu Ser Asp Thr Thr Ile Asn Val Met Lys Trp Lys Thr Val Ser Thr
50 55 60

Ile Phe Leu Val Val Val Leu Tyr Leu Ile Ile Gly Ala Thr Val Phe
65 70 75 80

Lys Ala Leu Glu Gln Pro His Glu Ile Ser Gln Arg Thr Thr Ile Val
85 90 95

Ile Gln Lys Gln Thr Phe Ile Ser Gln His Ser Cys Val Asn Ser Thr
100 105 110

Glu Leu Asp Glu Leu Ile Gln Gln Ile Val Ala Ala Ile Asn Ala Gly
115 120 125

Ile Ile Pro Leu Gly Asn Thr Ser Asn Gln Ile Ser His Trp Asp Leu
130 135 140

Gly Ser Ser Phe Phe Phe Ala Gly Thr Val Ile Thr Thr Ile Gly Phe
145 150 155 160

Gly Asn Ile Ser Pro Arg Thr Glu Gly Gly Lys Ile Phe Cys Ile Ile
165 170 175

Tyr Ala Leu Leu Gly Ile Pro Leu Phe Gly Phe Leu Leu Ala Gly Val
180 185 190

Gly Asp Gln Leu Gly Thr Ile Phe Gly Lys Gly Ile Ala Lys Val Glu
195 200 205

Asp Thr Phe Ile Lys Trp Asn Val Ser Gln Thr Lys Ile Arg Ile Ile
210 215 220

Ser Thr Ile Ile Phe Ile Leu Phe Gly Cys Val Leu Phe Val Ala Leu
225 230 235 240

Pro Ala Ile Ile Phe Lys His Ile Glu Gly Trp Ser Ala Leu Asp Ala
245 250 255

Ile Tyr Phe Val Val Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp Tyr
260 265 270

Val Ala Gly Gly Ser Asp Ile Glu Tyr Leu Asp Phe Tyr Lys Pro Val
275 280 285

Val Trp Phe Trp Ile Leu Val Gly Leu Ala Tyr Phe Ala Ala Val Leu
290 295 300

Ser Met Ile Gly Arg Leu Val Arg Val Ile Ser Lys Lys Thr Lys Glu
305 310 315 320

Glu Val Gly Glu Phe Arg Ala His Ala Ala Glu Trp Thr Ala Asn Val
325 330 335

Thr Ala Glu Phe Lys Glu Thr Arg Arg Arg Leu Ser Val Glu Ile Tyr
340 345 350

Asp Lys Phe Gln Arg Ala Thr Ser Ile Lys Arg Lys Leu Ser Ala Glu
355 360 365

Leu Ala Gly Asn His Asn Gln Glu Leu Thr Pro Cys Arg Arg Thr Leu
370 375 380

Ser Val Asn His Leu Thr Ser Glu Arg Asp Val Leu Pro Pro Leu Leu
385 390 395 400

Lys Thr Glu Ser Ile Tyr Leu Asn Gly Leu Ala Pro His Cys Ala Gly
405 410 415

Glu Glu Ile Ala Val Ile Glu Asn Ile Lys
420 425

<210> 46

<211> 2130

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (35)

<223> N AT POSITION 35 INDICATES UNDETERMINED
NUCLEOTIDE

<220>
<221> unsure
<222> (2057)
<223> N AT POSITION 2057 INDICATES UNDETERMINED
NUCLEOTIDE

<220>
<221> unsure
<222> (2067)
<223> N AT POSITION 2067 INDICATES UNDETERMINED
NUCLEOTIDE

<220>
<221> unsure
<222> (2111)
<223> N AT POSITION 2111 INDICATES UNDETERMINED
NUCLEOTIDE

<220>
<221> unsure
<222> (2120)
<223> N AT POSITION 2120 INDICATES UNDETERMINED
NUCLEOTIDE

*D
cont.*
<400> 46
ccatccta at acgactcact atagggctcg agcgncgc cggcagtaa aatgcctgcc 60
cgtgcagctc ggagcgcgca gcccgtctc gaataagaag tgagtacaat ggcgtgtttg 120
taaaaaaaaaaag cttcaagtcc gtcttttca aaaaacattt tgaatgctgc atgcctcatg 180
cttccccagcg cctcgccgga gagaccggc tataagcag gagtggccg acctgacttg 240
ctggatccta aatctgcccgc tcagaactcc aaaccgaggc tctcatttc cacgaaaccc 300
acagtgcctg cttcccggtt ggagagtgc acgaccatta atgttatgaa atggaagacg 360
gtctccacga tattcttgtt ggttgcctc tatctgatca tcggagccac cgtgttcaaa 420
gcattggagc agcctcatga gattcacag aggaccacca ttgtgatcca gaagcaaaca 480
ttcatatccc aacattcctg tgtcaattcg acggagctgg atgaactcat tcagcaaata 540
gtggcagcaa taaatgcagg gattataccg ttaggaaaca cctcaatca aatcagtcac 600
tgggatttgg gaagttcctt cttcttgct ggcactgtt ttacaaccat aggatttgg 660
aacatctcac cacccacaga agccggcaaa atattctgta tcatactatgc cttactgg 720
attccccctt ttggtttctt ctggctgg gttggagatc agctaggcac catatttgg 780
aaaggaattt ccaaagtgg a gatacgtt attaagtgg atgttagtca gaccaagatt 840
cgcatcatct caacaatcat attatacta ttggctgt tactcttgc ggctctgc 900
gcgatcatat tcaaacaat agaaggctgg agtgcctgg acgcattta ttttgtgtt 960
atcaactcaa caactattgg atttggtgac tacgttgac gtggatccga tattgaatat 1020
ctggacttct ataagcctgt cgtgtgttc tggatcctt tagggcttgc ttactttgc 1080
gctgtcctga gcatgattgg gagattggc cgagtgataat ctaaaaagac aaaagaagag 1140
gtgggagatg tcagagcaca cgctgctgag tggacagcca acgtcacagc cgaattcaaa 1200
gaaaccagga ggcgactgag tgtggagatt tatgacaagt tccagcggc cacccatc 1260
aagcggaaagc tctcgccaga actggctgg aaccacaatc aggagctgac tccttgtagg 1320

aggaccctgt cagtgaacca cctgaccagc gagagggatg tcttgccctcc cttaactgaag 1380
actgagagta tctatctgaa tggtttggcg ccacactgtg ctggtaaga gattgctgt 1440
attgagaaca tcaaataagcc ctctcttaa ataaccttag gcatagccat aggtgaggac 1500
ttctctatgc tctttatgac tggtgcttgt agcattttt aaattgtgca tgagctaaa 1560
gggggaacaa aatagataca cccatcatgg tcatactatca tcaagagaat ttgaaattct 1620
gagccagcac tttcttctg atgatgctt tgaaacggcc cacttctt gatgagtgg 1680
atgacaagca atgtctgatg ctttgtgtg cccagactgt tttcctctt cttccctaa 1740
tgtgccataa ggcctcagaa tgaattgaga attgttctg gtaacaatgt agctttgagg 1800
gatcagttct taactttca gggtctacct aactgagcct agatatggac catttatgga 1860
tgacaacaat ttttttttg taaatgacaa gaaattctta tgcagccctt tacctaagaa 1920
atttctgtca gtgccttatac ttatgaagaa acagaacctc tctagcta at gtgtggttc 1980
tccttccctg ccccccccccc taggctcacc tctgcagtct tttaccccag ttctccctt 2040
tgaataccat accttgntgg aaacagnngt taaaatgact gaagtgatga tgccgaagat 2100
gaaatagatg ncaaattagn tggacattga 2130

<210> 47
<211> 27
<212> DNA
<213> Homo sapiens

D
cont.
<400> 47
aaaagatcta aaatgcttcc cagcgcc 27

<210> 48
<211> 27
<212> DNA
<213> Homo sapiens

<400> 48
aaagtgcacc tatttgatgt tctcaat 27

<210> 49
<211> 27
<212> DNA
<213> Homo sapiens

<400> 49
aaaaagctta aaatgcttcc cagcgcc 27

<210> 50
<211> 27
<212> DNA
<213> Homo sapiens

<400> 50
aaatctagac tatttgatgt tctcaat

27

<210> 51
<211> 534
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (262)
<223> N AT POSITION 262 INDICATES UNDETERMINED
NUCLEOTIDE

*D
ent.*
<400> 51
aacaaaaacc ttttttgtt tgaatggcct agagaggta agggatcccc tgacgaacag 60
gagcagagcc agctagaacc tgggcctggc cagt tcaagg ccaccagagg gcagccttct 120
gcggaggca gtattgggtt aggcaaggac cccagcagac atggactca gagctctcac 180
tgtccactga ctctctcttc tccaggttat gcccacatgg ccccactatac gccaggcgga 240
aaggccttct gcattgtctt antagccctt gggctgccag ctccttagc ttcgtggcc 300
accctgcgcc attgcctgct gcctgtgtc agccgcccac gtgcctgggt aecggtccac 360
tggcagctgt caccggccag ggctgcgtc ctgcaggcag ttgcactggg actgctgtg 420
gccagcagct ttgtgtctgct gccagcgtc gtgcgtgtgg gccttcaggg cgactgcagc 480
ctgctggggg ccgtctactt ctgcattcagc tcgctcagca ccattggcct gggg 534

<210> 52
<211> 956
<212> DNA
<213> Mus musculus

<400> 52
atgatacgt ttaatacgac tcactatagg gaatttggcc ctcgaggcca agaattcggc 60
acgaggagaa tgtgcgcacg ttggctctca tcgtgtgcac cttcacctac ctgctgggtt 120
gcgcgcgggt gttcgcacgca ctggagtcgg agccggagat gatcagcgg cagcggctgg 180
agctgcggca gctggagctg cggcgcgcgt acaacccatcg cgaggcgcc tacgaggagc 240
tggagcgcgt cgtgcgtgcgc ctcaagccgc acaaggccgg cgtgcagtgg cgcttcggcc 300
gctccttcta cttgcgcata accgtcatca ccaccatgg ctatggcat gggcgccca 360
gcacggacgg aggcaaggtg ttctgcgt tctacgcgtc gctgggcatac ccgctcacac 420
tagtcatgtt ccagagcctg ggtgaacgca tcaacaccc tcgtgaggtac ctgctgcacc 480
gtgccaagag gggctgggc atgcggcacg ccgaagtgtc catggccaac atggtgctca 540
tcggtttctgt gtcgtgcatac agcagcgtgt gcatcggcgc agctgccttc tcctactacg 600
agcgctggac tttcttccag gcctattact actgcttcat caccctcacc accatcggt 660
tcggcacta tgtggcgctg cagaaggacc aggccgtcga gacgcagccg cagtatgtgg 720
cttcagcttc gtgtacatcc tcacggcgtc acggtcatcg ggccttcctc aacctcggtgg 780
tgctgcgatt catgaccatg aacgcccagg acgagaagcg tgatgcggag caccgcgccc 840
tgctcacgca caacggccag gctgtcgcc tgggtggcct gagctgcctg agcggtagcc 900

tgggcgacgg cgtgcgtccc.cgcgaccagg tcacatgcgc tgcggccgca agctta 956

```
<210> 53
<211> 1055
<212> DNA
<213> Mus musculus
```

<220>
<221> unsure
<222> (247)
<223> N AT POSITION 247 INDICATES UNDETERMINED
NUCLEOTIDE

<220>
<221> unsure
<222> (593)
<223> N AT POSITION 593 INDICATES UNDETERMINED
NUCLEOTIDE

<220>
<221> unsure
<222> (952)
<223> N AT POSITION 952 INDICATES UNDETERMINED
NUCLEOTIDE

<400> 53
ctgaaaccat gggcccata cctgctcctg cttatggccc acctgctggc catgggcatt 60
ggggctgtgg tgcttcaggc cctggagggc cctccagctc gccacactcca ggcccaggta 120
caggctgaac tggcttagctt ccaggcagag cacagggcct gcttgccacc tgaggccctg 180
gaggagctgc taggtgcggt cctgagagca caggccccatg gagtttccag cctgggcaac 240
agctcanaga caagcaactg ggatctgccc tcagctctgc tgttcactgc cagcatcctc 300
accaccacccg gttatggcca catggccccca ctctcctcag gtggaaaggc cttctgtgtg 360
gtctatgcag cccttgggct gccagcctct ctagcaacttggctgcccct ggcgcactgc 420
ttgctgcctg tgttcagtcg cccaggtgac tgggttagcca ttgcgtggca gctggcacca 480
gctcaggtcg ctctgctaca ggcagcagga ctgggcctcc tggtgtgcctg tgtttcatcg 540
ctgctgccag cactggtgct gtgggggtgt a cagggtgact ggcagcctgc tanaaccatc 600
tacttctgtt tcggctcaact cagcacgatc ggccttaggag acttgctgcc tgcccatgga 660
cgtggcctgc acccagccat ttaccacctt gggcagtttgcacttcttgg ttacttgctc 720
ctggggcctcc tggccatgtt gttacgagta gagacccctt cagagctgcc tcaggtccgt 780
gccatggtga aattctttgg gcccagtgcc tctagaaccg atgaagatca agatggcattc 840
ctaggccaag atgagctggc tctgagcaact gtgctgcctg acgccccagt cttgggacca 900
accaccccaag cctgagcggg aggccaccaag gagtgcttga agaacatagc angaagggtt 960
atgggaatgaa atatgtcatg ggataatgtt aattttaaaa attaaatggg ctgcttagca 1020
tgcaaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaa 1055

<210> 54

<211> 178

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> (88)

<223> X AT POSITION 88 INDICATES UNDETERMINED RESIDUE

<400> 54

Asn Lys Asn Leu Phe Cys Phe Glu Trp Pro Arg Glu Gly Lys Gly Ser
1 5 10 15

Pro Asp Glu Gln Glu Gln Ser Gln Leu Glu Pro Gly Pro Gly Gln Phe
20 25 30

Lys Ala Thr Arg Gly Gln Pro Ser Ala Glu Gly Ser Ile Gly Val Gly
35 40 45

Arg Asp Pro Ser Arg His Gly Thr Gln Ser Ser His Cys Pro Leu Thr
50 55 60

Leu Ser Ser Pro Gly Tyr Gly His Met Ala Pro Leu Ser Pro Gly Gly
65 70 75 80

Lys Ala Phe Cys Met Val Leu Xaa Ala Leu Gly Leu Pro Ala Ser Leu
85 90 95

Ala Leu Val Ala Thr Leu Arg His Cys Leu Leu Pro Val Leu Ser Arg
100 105 110

Pro Arg Ala Trp Val Ala Val His Trp Gln Leu Ser Pro Ala Arg Ala
115 120 125

Ala Leu Leu Gln Ala Val Ala Leu Gly Leu Leu Val Ala Ser Ser Phe
130 135 140

Val Leu Leu Pro Ala Leu Val Leu Trp Gly Leu Gln Gly Asp Cys Ser
145 150 155 160

Leu Leu Gly Ala Val Tyr Phe Cys Phe Ser Ser Leu Ser Thr Ile Gly
165 170 175

Leu Gly

<210> 55

<211> 309

<212> PRT

<213> Mus musculus

<400> 55

Gly Ile Trp Pro Ser Arg Pro Arg Ile Arg His Glu Glu Asn Val Arg
1 5 10 15

Thr Leu Ala Leu Ile Val Cys Thr Phe Thr Tyr Leu Leu Val Gly Ala
20 25 30

Ala Val Phe Asp Ala Leu Glu Ser Glu Pro Glu Met Ile Glu Arg Gln
35 40 45

Arg Leu Glu Leu Arg Gln Leu Glu Leu Arg Ala Arg Tyr Asn Leu Ser
50 55 60

Glu Gly Gly Tyr Glu Glu Leu Glu Arg Val Val Leu Arg Leu Lys Pro
65 70 75 80

His Lys Ala Gly Val Gln Trp Arg Phe Ala Gly Ser Phe Tyr Phe Ala
85 90 95

Ile Thr Val Ile Thr Thr Ile Gly Tyr Gly His Ala Ala Pro Ser Thr
100 105 110

Asp Gly Gly Lys Val Phe Cys Met Phe Tyr Ala Leu Leu Gly Ile Pro
115 120 125

Leu Thr Leu Val Met Phe Gln Ser Leu Gly Glu Arg Ile Asn Thr Ser
130 135 140

Val Arg Tyr Leu Leu His Arg Ala Lys Arg Gly Leu Gly Met Arg His
145 150 155 160

Ala Glu Val Ser Met Ala Asn Met Val Leu Ile Gly Phe Val Ser Cys
165 170 175

Ile Ser Thr Leu Cys Ile Gly Ala Ala Ala Phe Ser Tyr Tyr Glu Arg
180 185 190

Trp Thr Phe Phe Gln Ala Tyr Tyr Cys Phe Ile Thr Leu Thr Thr
195 200 205

Ile Gly Phe Gly Asp Tyr Val Ala Leu Gln Lys Asp Gln Ala Leu Gln
210 215 220

Thr Gln Pro Gln Tyr Val Ala Ser Ala Ser Cys Thr Ser Ser Arg Ala

225

230

235

240

His Gly His Arg Arg Phe Leu Asn Leu Val Val Leu Arg Phe Met Thr
245 250 255

Met Asn Ala Glu Asp Glu Lys Arg Asp Ala Glu His Arg Ala Leu Leu
260 265 270

Thr His Asn Gly Gln Ala Val Gly Leu Gly Gly Leu Ser Cys Leu Ser
275 280 285

Gly Ser Leu Gly Asp Gly Val Arg Pro Arg Asp Pro Val Thr Cys Ala
290 295 300

Ala Ala Ala Ser Leu
305

<210> 56

<211> 304

<212> PRT

<213> Mus musculus

D'unk.
<220>

<221> UNSURE

<222> (83)

<223> N AT POSITION 83 INDICATES UNDETERMINED RESIDUE

<220>

<221> UNSURE

<222> (198)

<223> N AT POSITION 198 INDICATES UNDETERMINED RESIDUE

<400> 56

Leu Lys Pro Trp Ala Arg Tyr Leu Leu Leu Met Ala His Leu Leu
1 5 10 15

Ala Met Gly Leu Gly Ala Val Val Leu Gln Ala Leu Glu Gly Pro Pro
20 25 30

Ala Arg His Leu Gln Ala Gln Val Gln Ala Glu Leu Ala Ser Phe Gln
35 40 45

Ala Glu His Arg Ala Cys Leu Pro Pro Glu Ala Leu Glu Glu Leu Leu
50 55 60

Gly Ala Val Leu Arg Ala Gln Ala His Gly Val Ser Ser Leu Gly Asn
65 70 75 80

Ser Ser Xaa Thr Ser Asn Trp Asp Leu Pro Ser Ala Leu Leu Phe Thr
85 90 95

Ala Ser Ile Leu Thr Thr Gly Tyr Gly His Met Ala Pro Leu Ser
100 105 110

Ser Gly Gly Lys Ala Phe Cys Val Val Tyr Ala Ala Leu Gly Leu Pro
115 120 125

Ala Ser Leu Ala Leu Val Ala Ala Leu Arg His Cys Leu Leu Pro Val
130 135 140

Phe Ser Arg Pro Gly Asp Trp Val Ala Ile Arg Trp Gln Leu Ala Pro
145 150 155 160

Ala Gln Ala Ala Leu Leu Gln Ala Ala Gly Leu Gly Leu Leu Val Ala
165 170 175

Cys Val Phe Met Leu Leu Pro Ala Leu Val Leu Trp Gly Val Gln Gly
180 185 190

Asp Trp Gln Pro Ala Xaa Thr Ile Tyr Phe Cys Phe Gly Ser Leu Ser
195 200 205

Thr Ile Gly Leu Gly Asp Leu Leu Pro Ala His Gly Arg Gly Leu His
210 215 220

Pro Ala Ile Tyr His Leu Gly Gln Phe Ala Leu Leu Gly Tyr Leu Leu
225 230 235 240

Leu Gly Leu Leu Ala Met Leu Leu Ala Val Glu Thr Phe Ser Glu Leu
245 250 255

Pro Gln Val Arg Ala Met Val Lys Phe Phe Gly Pro Ser Gly Ser Arg
260 265 270

Thr Asp Glu Asp Gln Asp Gly Ile Leu Gly Gln Asp Glu Leu Ala Leu
275 280 285

Ser Thr Val Leu Pro Asp Ala Pro Val Leu Gly Pro Thr Thr Pro Ala
290 295 300

<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> VARIANT
<222> (1)...(9)
<223> X AT POSITIONS 1, 4, AND 5 IS T OR S; X AT POSITION 6 IS I OR V; X AT POSITIONS 2, 3, AND 8 IS Y, F, V, I, M, OR L

<220>
<223> Description of Artificial Sequence: POTASSIUM ION CHANNEL SEQUENCE

<400> 57
Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Gly
1 5

D
only.
<210> 58
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: POTASSIUM ION CHANNEL SEQUENCE

<220>
<221> VARIANT
<222> (1)...(8)
<223> X AT POSITION 1 IS Y OR F; X AT POSITION 2 IS A, S, OR G; X AT POSITIONS 3, 4, 6, AND 8 ARE M, I, V, L, F, OR Y

<400> 58
Xaa Xaa Xaa Xaa Gly Xaa Pro Xaa
1 5

<210> 59
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: POTASSIUM ION

CHANNEL SEQUENCE

<400> 59
Tyr Ala Leu Leu Gly Ile Pro
1 5

<210> 60
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: POTASSIUM ION
CHANNEL SEQUENCE

<220>
<221> VARIANT
<222> (6)
<223> X AT POSITION 6 IS M, I, V, L, F, OR Y

<400> 60
Tyr Ala Leu Leu Gly Xaa Pro
1 5

D
ent
<210> 61.
<211> 178
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (88)
<223> X AT POSITION 88 INDICATES UNDETERMINED RESIDUE

<400> 61
Asn Lys Asn Leu Phe Cys Phe Glu Trp Pro Arg Glu Gly Lys Gly Ser
1 5 10 15

Pro Asp Glu Gln Glu Gln Ser Gln Leu Glu Pro Gly Pro Gly Gln Phe
20 25 30

Lys Ala Thr Arg Gly Gln Pro Ser Ala Glu Gly Ser Ile Gly Val Gly
35 40 45

Arg Asp Pro Ser Arg His Gly Thr Gln Ser Ser His Cys Pro Leu Thr
50 55 60

Leu Ser Ser Pro Gly Tyr Gly His Met Ala Pro Leu Ser Pro Gly Gly
65 70 75 80

Lys Ala Phe Cys Met Val Leu Xaa Ala Leu Gly Leu Pro Ala Ser Leu
85 90 95

Ala Leu Val Ala Thr Leu Arg His Cys Leu Leu Pro Val Leu Ser Arg
100 105 110

Pro Arg Ala Trp Val Ala Val His Trp Gln Leu Ser Pro Ala Arg Ala
115 120 125

Ala Leu Leu Gln Ala Val Ala Leu Gly Leu Leu Val Ala Ser Ser Phe
130 135 140

Val Leu Leu Pro Ala Leu Val Leu Trp Gly Leu Gln Gly Asp Cys Ser
145 150 155 160

Leu Leu Gly Ala Val Tyr Phe Cys Phe Ser Ser Leu Ser Thr Ile Gly
165 170 175

Leu Gly

D
cont.
<210> 62
<211> 309
<212> PRT
<213> Mus musculus

<400> 62
Gly Ile Trp Pro Ser Arg Pro Arg Ile Arg His Glu Glu Asn Val Arg
1 5 10 15

Thr Leu Ala Leu Ile Val Cys Thr Phe Thr Tyr Leu Leu Val Gly Ala
20 25 30

Ala Val Phe Asp Ala Leu Glu Ser Glu Pro Glu Met Ile Glu Arg Gln
35 40 45

Arg Leu Glu Leu Arg Gln Leu Glu Leu Arg Ala Arg Tyr Asn Leu Ser
50 55 60

Glu Gly Gly Tyr Glu Glu Leu Glu Arg Val Val Leu Arg Leu Lys Pro
65 70 75 80

His Lys Ala Gly Val Gln Trp Arg Phe Ala Gly Ser Phe Tyr Phe Ala

85

90

95

Ile Thr Val Ile Thr Thr Ile Gly Tyr Gly His Ala Ala Pro Ser Thr
 100 105 110

Asp Gly Gly Lys Val Phe Cys Met Phe Tyr Ala Leu Leu Gly Ile Pro
 115 120 125

Leu Thr Leu Val Met Phe Gln Ser Leu Gly Glu Arg Ile Asn Thr Ser
 130 135 140

Val Arg Tyr Leu Leu His Arg Ala Lys Arg Gly Leu Gly Met Arg His
 145 150 155 160

Ala Glu Val Ser Met Ala Asn Met Val Leu Ile Gly Phe Val Ser Cys
 165 170 175

Ile Ser Thr Leu Cys Ile Gly Ala Ala Ala Phe Ser Tyr Tyr Glu Arg
 180 185 190

Trp Thr Phe Phe Gln Ala Tyr Tyr Cys Phe Ile Thr Leu Thr Thr
 195 200 205

Ile Gly Phe Gly Asp Tyr Val Ala Leu Gln Lys Asp Gln Ala Leu Gln
 210 215 220

Thr Gln Pro Gln Tyr Val Ala Ser Ala Ser Cys Thr Ser Ser Arg Ala
 225 230 235 240

His Gly His Arg Arg Phe Leu Asn Leu Val Val Leu Arg Phe Met Thr
 245 250 255

Met Asn Ala Glu Asp Glu Lys Arg Asp Ala Glu His Arg Ala Leu Leu
 260 265 270

Thr His Asn Gly Gln Ala Val Gly Leu Gly Gly Leu Ser Cys Leu Ser
 275 280 285

Gly Ser Leu Gly Asp Gly Val Arg Pro Arg Asp Pro Val Thr Cys Ala
 290 295 300

Ala Ala Ala Ser Leu
 305

<210> 63
 <211> 434
 <212> PRT

<213> *Caenorhabditis elegans*

<400> 63

Met Val Ile Ile Asn Arg Ser Asn Thr Tyr Ala Val Glu Gln Glu Ala
1 5 10 15

Phe Pro Arg Asp Lys Tyr Asn Ile Val Tyr Trp Leu Val Ile Leu Val
20 25 30

Gly Phe Gly Val Leu Leu Pro Trp Asn Met Phe Ile Thr Ile Ala Pro
35 40 45

Glu Tyr Tyr Val Asn Tyr Trp Phe Lys Pro Asp Gly Val Glu Thr Trp
50 55 60

Tyr Ser Lys Glu Phe Met Gly Ser Leu Thr Ile Gly Ser Gln Leu Pro
65 70 75 80

Asn Ala Ser Ile Asn Val Phe Asn Leu Phe Leu Ile Ile Ala Gly Pro
85 90 95

Leu Ile Tyr Arg Val Phe Ala Pro Val Cys Phe Asn Ile Val Asn Leu
100 105 110

Thr Ile Ile Leu Ile Leu Val Ile Val Leu Glu Pro Thr Glu Asp Ser
115 120 125

Met Ser Trp Phe Phe Trp Val Thr Leu Gly Met Ala Thr Ser Ile Asn
130 135 140

Phe Ser Asn Gly Leu Tyr Glu Asn Ser Val Tyr Gly Val Gly Gly Asp
145 150 155 160

Phe Pro His Thr Tyr Ile Gly Ala Leu Leu Ile Gly Asn Asn Ile Cys
165 170 175

Gly Leu Leu Ile Thr Val Val Lys Ile Gly Val Thr Tyr Phe Leu Asn
180 185 190

Asp Glu Pro Lys Leu Val Ala Ile Val Tyr Phe Gly Ile Ser Leu Val
195 200 205

Ile Leu Leu Val Cys Ala Ile Ala Leu Phe Phe Ile Thr Lys Gln Asp
210 215 220

Phe Tyr His Tyr His His Gln Lys Gly Met Glu Ile Arg Glu Lys Ala
225 230 235 240

Glu Thr Asp Arg Pro Ser Pro Ser Ile Leu Trp Thr Thr Phe Thr Asn
245 250 255

Cys Tyr Gly Gln Leu Phe Asn Val Trp Phe Cys Phe Ala Val Thr Leu
260 265 270

Thr Ile Phe Pro Val Met Met Thr Val Thr Thr Arg Gly Asp Ser Gly
275 280 285

Phe Leu Asn Lys Ile Met Ser Glu Asn Asp Glu Ile Tyr Thr Leu Leu
290 295 300

Thr Ser Phe Leu Val Phe Asn Leu Phe Ala Ala Ile Gly Ser Ile Val
305 310 315 320

Ala Ser Lys Ile His Trp Pro Thr Pro Arg Tyr Leu Lys Phe Ala Ile
325 330 335

Ile Leu Arg Ala Leu Phe Ile Pro Phe Phe Phe Cys Asn Tyr Arg
340 345 350

Val Gln Thr Arg Ala Tyr Pro Val Phe Phe Glu Ser Thr Asp Ile Phe
355 360 365

Val Ile Gly Gly Ile Ala Met Ser Phe Ser His Gly Tyr Leu Ser Ala
370 375 380

Leu Ala Met Gly Tyr Thr Pro Asn Val Val Pro Ser His Tyr Ser Arg
385 390 395 400

Phe Ala Ala Gln Leu Ser Val Cys Thr Leu Met Val Gly Leu Leu Thr
405 410 415

Gly Gly Leu Trp Pro Val Val Ile Glu His Phe Val Asp Lys Pro Ser
420 425 430

Ile Leu

<210> 64

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: POTASSIUM ION
CHANNEL SEQUENCE

<220>
<221> VARIANT
<222> (1)...(7)
<223> X AT POSITION 1 IS Y OR F; X AT POSITION 2 IS A,
S, OR G; X AT POSITIONS 3, 4, AND 6 ARE M, I, V,
L, F, OR Y

<400> 64
Xaa Xaa Xaa Xaa Gly Xaa Pro
1 5

<210> 65
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus
sequence between Ce orf1 and Dm orf1

D
cont
<400> 65
Thr Trp Thr Phe
1

<210> 66
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: consensus
sequence between Ce orf1 and Dm orf1

<400> 66
Gly Tyr Gly Asn
1

<210> 67
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: consensus

~~sequence between Ce orf1 and Dm orf1~~

<400> 67
Gly Phe Gly Asp
1

~~but~~
62

D'
uncl.